Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=10; day=21; hr=13; min=23; sec=38; ms=121;
]

Validated By CRFValidator v 1.0.3

Application No: 10643589 Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-15 11:59:56.021 **Finished:** 2008-09-15 11:59:56.934

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 913 ms

Total Warnings: 10
Total Errors: 1

No. of SeqIDs Defined: 13

Actual SeqID Count: 13

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (1)
W	402	Undefined organism found in <213> in SEQ ID (2)
W	402	Undefined organism found in <213> in SEQ ID (3)
W	402	Undefined organism found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
E	257	Invalid sequence data feature in <221> in SEQ ID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
W	213	Artificial or Unknown found in <213> in SEQ ID (13)

SEQUENCE LISTING

<110> PITTMAN, DEBRA D.	
<120> COMPOSITIONS AND METHODS FOR TREATING RAGE-ASSOCIATED DISORDERS	
<130> WYTH-P01-002	
<140> 10643589	
<141> 2003-08-18	
<150> 60/404,205	
<151> 2002-08-16	
<160> 13	
<170> PatentIn version 3.5	
<210> 1	
<211> 2057	
<212> DNA	
<213> Mus sp.	
<220>	
<223> Murine Soluble RAGE_FC	
<400> 1	
atgccagcgg ggacagcagc tagagcctgg gtgctggttc ttgctctatg gggagctgta	60
gctggtggtc agaacatcac agcccggatt ggagagccac ttgtgctaag ctgtaagggg	120
gerggrygee agaacareae ageeeggare ggagageeae regryeraag ergraagggg	120
gcccctaaga agccgcccca gcagctagaa tggaaactga acacaggaag aactgaagct	180
tggaaggtcc tctctcccca gggaggcccc tgggacagcg tggctcaaat cctccccaat	240
ggttccctcc tccttccagc cactggaatt gtcgatgagg ggacgttccg gtgtcgggca	300
actaacaggc gagggaagga ggtcaagtcc aactaccgag tccgagtcta ccagattcct	360
gggaagccag aaattgtgga teetgeetet gaacteacag eeagtgteee taataaggtg	420
	400
gggacatgtg tgtctgaggg aagctaccct gcagggaccc ttagctggca cttagatggg	480
assertates transpared assertates as a second as	540
aaacttetga tteeegatgg caaagaaaca etegtgaagg aagagaeeag gagaeaeeet	240
gagacgggac tetttacaet geggteagag etgaeagtga tececaecea aggaggaace	600
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
acccatecta cetteteetg cagtiteage etgggeette eeeggegeag acceetgaae	660
acagececta tecaacteeg agteagggag eetgggeete eagagggeat teagetgttg	720

gttgagcctg aaggtggaat agtcgctcct ggtgggactg tgaccttgac ctgtgccatc

tctgcccagc cccctcctca ggtccactgg ataaaggatg gtgcaccctt gcccctggct

780

900 cccagccctg tgctgctcct ccctgaggtg gggcacgcgg atgagggcac ctatagctgc gtggccaccc accctagcca cggacctcag gaaagccctc ctgtcagcat cagggtcaca 960 gaaaccggcg atgagggcc agctgaaggc tctgtgggtg agtctgggct gggtacgcta 1020 1080 gccctggccg agccccgcgg accgacaatc aagccctgtc ctccatgcaa atgcccaggt aagtcactag accagagete cacteeeggg agaatggtaa gtgetataaa cateeetgea 1140 ctagaggata agccatgtca agatccattt ccatctctc tcatcagcac ctaacctcga 1200 gggtggacca tccgtcttca tcttccctcc aaagatcaag gatgtactca tgatctccct 1260 gagccccata gtcacatgtg tggtggtgga tgtgagcgag gatgacccag atgtccagat 1320 cagctggttt gtgaacaacg tggaagtaca cacagctcag acacaaaccc atagagagga 1380 ttacaacagt actctccggg tggtcagtgc cctccccatc cagcaccagg actggatgag 1440 1500 tggcaagget ttegcatgeg eegteaacaa caaagaeete eeagegeeea tegagagaae catctcaaaa cccaaaggtg agagctgcag cctgactgca tgggggctgg gatgggcata 1560 aggataaagg tetgtgtgga cageettetg etteageeat gaeetttgtg tatgttteta 1620 ccctcacagg gtcagtaaga gctccacagg tatatgtctt gcctccacca gaagaagaga 1680 tgactaagaa acaggtcact ctgacctgca tggtcacaga cttcatgcct gaagacattt 1740 acgtggagtg gaccaacaac gggaaaacag agctaaacta caagaacact gaaccagtcc 1800 tggactctga tggttcttac ttcatgtaca gcaagctgag agtggaaaag aagaactggg 1860 tggaaagaaa tagctactcc tgttcagtgg tccacgaggg tctgcacaat caccacacga ctaagagctt ctcccggact ccgggtaaat gagctcagca cccacaaaac tctcaggtcc 1980 aaagagacac ccacactcat ctccatgctt cccttgtata aataaagcac ccagcaatgc 2040 ctgggaccat gtaatag 2057

<210> 2

<211> 343

<212> PRT

<213> Mus sp.

<220>

<223> Murine Soluble RAGE_FC

<400> 2

Met Pro Ala Gly Thr Ala Ala Arg Ala Trp Val Leu Val Leu Ala Leu 1 5 10 15

Trp Gly Ala	a Val Ala 20	. Gly Gly	Gln As		Thr Ala	-	le Gly	Glu
Pro Leu Vai	l Leu Ser	Cys Lys	Gly Al	la Pro I	Lys Lys	Pro P 45	ro Gln	Gln
Leu Glu Trp 50	o Lys Leu	Asn Thr	Gly Ai	rg Thr (Glu Ala 60	Trp L	ys Val	Leu
Ser Pro Glr	n Gly Gly	Pro Trp	Asp Se		Ala Gln 75	Ile L	eu Pro	Asn 80
Gly Ser Le	ı Leu Leu 85	Pro Ala	Thr G	ly Ile v 90	Val Asp	Glu G	ly Thr 95	Phe
Arg Cys Arg	g Ala Thr 100	Asn Arg		ly Lys (05	Glu Val		er Asn 10	Tyr
Arg Val Arg	_	Gln Ile	Pro Gl	ly Lys I	Pro Glu	Ile V 125	al Asp	Pro
Ala Ser Glu	ı Leu Thr	Ala Ser		ro Asn I	Lys Val 140	Gly T	hr Cys	Val
Ser Glu Gly 145	7 Ser Tyr	Pro Ala	Gly Th		Ser Trp 155	His L	eu Asp	Gly 160
Lys Leu Leu	ı Ile Pro 165		Lys Gl	lu Thr 1	Leu Val	Lys G	lu Glu 175	Thr
Arg Arg Hi:	s Pro Glu 180	Thr Gly		he Thr 1 85	Leu Arg		lu Leu 90	Thr
Val Ile Pro		Gly Gly	Thr Th	hr His I	Pro Thr	Phe S	er Cys	Ser
Phe Ser Leu 210	ı Gly Leu	Pro Arg 215	-	rg Pro 1	Leu Asn 220	Thr A	la Pro	Ile
Gln Leu Arç	g Val Arg	Glu Pro 230	Gly Pi		Glu Gly 235	Ile G	ln Leu	Leu 240

Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu 245 250 255

Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
260 265 270

Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Pro 275 280 285

Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His 290 295 300

Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr 305 310 315 320

Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly 325 330 335

Leu Gly Thr Leu Ala Leu Ala 340

<210> 3

<211> 1810

<212> DNA

<213> Mus sp.

<220>

<223> Murine solTNFRII_FC

<400> 3

atggcgcccg ccgccctctg ggtcgcgctg gtcttcgaac tgcagctgtg ggccaccggg 60 cacacagtgc ccgcccaggt tgtcttgaca ccctacaaac cggaacctgg gtacgagtgc cagateteac aggaatacta tgacaggaag geteagatgt getgtgetaa gtgteeteet 180 ggccaatatg tgaaacattt ctgcaacaag acctcggaca ctgtgtgtgc ggactgtgag 240 gcaagcatgt atacccaggt ctggaaccag tttcgtacat gtttgagctg cagttcttcc 300 tgtagcactg accaggtgga gacccgcgcc tgcactaaac agcagaaccg agtgtgtgct 360 tgcgaagctg gcaggtactg cgccttgaaa acccattctg gcagctgtcg acagtgcatg 420 aggctgagca agtgcggccc tggcttcgga gtggccagtt caagagcccc aaatggaaat 480 540 gtgctatgca aggcctgtgc cccagggacg ttctctgaca ccacatcatc cacagatgtg 600 tgcaggcccc accgcatctg tagcatcctg gctattcccg gaaatgcaag cacagatgca

gtctgtgcgc ccgagtcccc aactctaagt gccatcccaa ggacactcta cgtatctcag 660 ccagagccca caagatccca acccctggat caagagccag ggcccagcca aactccaagc 720 atccttacat cgttgggttc aacccccatt attgaacaaa gtaccaaggg tggcgagccc 780 840 cgcggaccga caatcaagcc ctgtcctcca tgcaaatgcc caggtaagtc actagaccag agetecacte eegggagaat ggtaagtget ataaacatee etgeactaga ggataageea 900 960 tgtacagatc catttccatc tctcctcatc agcacctaac ctcgagggtg gaccatccgt cttcatcttc cctccaaaga tcaaggatgt actcatgatc tccctgagcc ccatagtcac 1020 1080 atgtgtggtg gtggatgtga gcgaggatga cccagatgtc cagatcagct ggtttgtgaa caacgtggaa gtacacacag ctcagacaca aacccataga gaggattaca acagtactct 1140 ccgggtggtc agtgccctcc ccatccagca ccaggactgg atgagtggca aggctttcgc 1200 atgcgccgtc aacaacaaag acctcccagc gcccatcgag agaaccatct caaaacccaa 1260 aggtgagagc tgcagcctga ctgcatgggg gctgggatgg gcataaggat aaaggtctgt 1320 gtggacagcc ttctgcttca gccatgacct ttgtgtatgt ttctaccctc acagggtcag 1380 taagagctcc acaggtatat gtcttgcctc caccagaaga agagatgact aagaaacagg 1440 tcactctgac ctgcatggtc acagacttca tgcctgaaga catttacgtg gagtggacca 1500 acaacgggaa aacagagcta aactacaaga acactgaacc agtcctggac tctgatggtt 1560 cttacttcat gtacagcaag ctgagagtgg aaaagaagaa ctgggtggaa agaaatagct 1620 actectgtte agtggtecae gagggtetge acaateaeca caegaetaag agetteteee qgactccqqq taaatqaqct caqcacccac aaaactctca qqtccaaaqa qacacccaca 1740 ctcatctcca tgcttccctt gtataaataa agcacccagc aatgcctggg accatgtaat 1800 aggaattatc 1810

<210> 4

<211> 258

<212> PRT

<213> Mus sp.

<220>

<223> Murine solTNFRII_FC

<400> 4

Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu 15

Trp Ala Thr	Gly His	Thr Val		Ala Gln 25	Val Val	Leu	Thr 30	Pro	Tyr
Lys Pro Glu 35	Pro Gly	Tyr Glu	Cys 0	Gln Ile	Ser Gln	Glu 45	Tyr	Tyr	Asp
Arg Lys Ala 50	Gln Met	Cys Cys 55	Ala I	Lys Cys	Pro Pro 60	Gly	Gln	Tyr	Val
Lys His Phe 65	Cys Asn	Lys Thr	Ser A	Asp Thr	Val Cys 75	Ala	Asp	Cys	Glu 80
Ala Ser Met	Tyr Thr 85	Gln Val	Trp A	Asn Gln 90	Phe Arg	Thr	Суз	Leu 95	Ser
Cys Ser Ser	Ser Cys 100	Ser Thr	_	Gln Val 105	Glu Thr	Arg	Ala 110	Cys	Thr
Lys Gln Gln 115	Asn Arg	Val Cys	Ala 0	Cys Glu	Ala Gly	Arg 125	Tyr	Cys	Ala
Leu Lys Thr 130	His Ser	Gly Ser 135	Cys A	Arg Gln	Cys Met 140	Arg	Leu	Ser	Lys
Cys Gly Pro 145	Gly Phe	Gly Val 150	Ala S	Ser Ser	Arg Ala 155	Pro	Asn	Gly	Asn 160
Val Leu Cys	Lys Ala 165	Cys Ala	Pro 0	Gly Thr 170	Phe Ser	Asp	Thr	Thr 175	Ser
Ser Thr Asp	Val Cys 180	Arg Pro		Arg Ile 185	Cys Ser	Ile	Leu 190	Ala	Ile
Pro Gly Asn 195	Ala Ser	Thr Asp	Ala V 200	Val Cys	Ala Pro	Glu 205	Ser	Pro	Thr
Leu Ser Ala 210	Ile Pro	Arg Thr 215	Leu 7	Tyr Val	Ser Gln 220	Pro	Glu	Pro	Thr
Arg Ser Gln 225	Pro Leu	Asp Gln 230	Glu F	Pro Gly	Pro Ser 235	Gln	Thr	Pro	Ser 240

```
Ile Leu Thr Ser Leu Gly Ser Thr Pro Ile Ile Glu Gln Ser Thr Lys
245 250 255
```

Gly Gly

<210> 5

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Human RAGE-LBE fused to an Fc element

<220>

<221> MOD_RES

<222> (423)..(423)

<223> Any amino acid

<400> 5

Met Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu 1 5 10 15

Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
20 25 30

Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg 35 40 45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu 50 55 60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro 65 70 75 80

As Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile 85 90 95

Phe Arg Cys Gln Ala Asn Ile Asn Arg Asn Gly Lys Glu Thr Lys Ser 100 105 110

Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro Glu Lys Pro Glu Ile Val 115 120 125

Asp Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr

130 135 140

Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu 145 150 155 160 Asp Gly Lys Pro Leu Val Leu Asn Glu Lys Gly Val Ser Val Lys Glu 165 170 Gln Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu 185 190 Leu Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser 195 200 205 Cys Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala 210 215 220 Pro Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln 230 235 240 Leu Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val 245 250 255 Thr Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp 260 265 Met Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile 275 280 285 Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala 290 295 300 Thr His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser 305 315 310 Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly 325 330 335 Ser Gly Leu Gly Thr Leu Ala Leu Ala Cys Ala Gly Ser Gly Ser Gly 345 350 340

Ser Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

365

360

Pro	Ala 370	Pro	Glu	Ala	Leu	Gly 375	Ala	Pro	Ser	Val	Phe 380	Leu	Phe	Pro	Asp
Lys 385	Pro	Lys	Asp	Thr	Leu 390	Met	Ile	Ser	Arg	Thr 395	Pro	Glu	Val	Thr	Cys 400
Val	Val	Val	Asp	Val 405	Ser	His	Glu	Asp	Pro 410	Glu	Val	Lys	Phe	Asn 415	Trp
Tyr	Val	Asp	Gly 420	Val	Glu	Xaa	Gln	Asn 425	Ala	Lys	Thr	Lys	Pro 430	Arg	Glu
Glu	Gln	Tyr 435	Asn	Ser	Thr	Tyr	Arg 440	Val	Val	Ser	Val	Leu 445	Thr	Val	Leu
His	Gln 450	Asp	Trp	Leu	Asn	Gly 455	Lys	Glu	Tyr	Lys	Cys 460	Lys	Val	Ser	Asn
Lys 465	Ala	Leu	Pro	Ala	Pro 470	Ile	Glu	Lys	Thr	Ile 475	Ser	Lys	Ala	Lys	Gly 480
Gln	Pro	Arg	Glu	Pro 485	Gln	Val	Tyr	Thr	Leu 490	Pro	Pro	Ser	Arg	Glu 495	Glu
Met	Thr	Lys	Asn 500	Gln	Val	Ser	Leu	Thr 505	Cys	Leu	Val	Lys	Gly 510	Phe	Tyr
Pro	Ser	Asp 515	Ile	Ala	Val	Glu	Trp 520	Glu	Ser	Asn	Gly	Gln 525	Pro	Glu	Asn
Lys	Cys 530	Lys	Thr	Thr	Pro	Pro 535	Val	Leu	Asp	Ser	Asp 540	Gly	Ser	Phe	Phe
Leu 545	Tyr	Ser	Lys	Leu	Thr 550	Asp	Lys	Ser	Arg	Trp 555	Gln	Gln	Gly	Asn	Val 560
Phe	Ser	Cys	Ser	Val 565	Met	His	Glu	Ala	Leu 570	His	Asn	His	Tyr	Thr 575	Gln
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							

<210> 6 <211> 1761 <212> DNA <213> Artificial Sequence

ttcccccaa aacccaagga caccctcatg at

<220>

<223> Description of Artificial Sequence: Synthetic Human RAGE-LBE fused to an Fc element

<400> 6 atggcagccg gaacagcagt tggagcctgg gtgctggtcc tcagtctgtg gggggcagta 60 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgtaagggg 120 180 gcccccaaga aaccacccca gcggctggaa tggaaactga acacaggccg gacagaagct tggaaggtcc tgtctcccca gggaggaggc ccctgggaca gtgtggctcg tgtccttccc 240 aacggetece tetteettee ggetgteggg atceaggatg aggggatttt ceggtgeeag 300 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt 360 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tcccaataag 420 gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat 480 540 gggaagcccc tggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac cctgagacag ggctcttcac actgcagtcg gagctaatgg tgaccccagc ccggggagga 600 gateceegte ceacettete etgtagette ageceaggee tteecegaea eegggeettg 660 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg 720 gtggtggagc cagaaggtgg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa 780 gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgcccctt 840 900 cccccagcc ctgtgctgat cctccctgag atagggcctc aggaccaggg aacctacagc 960 tgtgtggcca cccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc ategaaccag gegaggaggg gecaactgea ggetetgtgg gaggateagg getgggaact 1020 ctagccctgg cctgcgcagg tagcggctcc ggaagtgggg agcccaaatc ttgtgacaaa 1080 actcacacat gcccaccgtg cccagcacct gaagccctgg gggcaccgtc agtcttcctc 1140